Aggressiveness traits, fitness and insights in their genetic basis in *Magnaporthe oryzae*

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Partial resistance is often presented as an alternative to the frequent failure of complete and specific resistance of plants to pathogens. Partial resistance is presumed to be non-specific and multigenic. On the pathogen side aggressiveness traits are presumed to be polygenic. However, experimental evidences are still limited. We thus developed some experimental work on genotype x genotype (GxG) interactions and on the genetics of aggressiveness in the rice - *Magnaporthe oryzae* pathosystem. We inoculated 18 different genotypes of the fungus *M. oryzae* on three rice plant varieties showing different levels of partial resistance. We estimated the success of each plant-fungus interaction by measuring fungal fitness (total number of spores) and three fungal life history traits: the infection success (number of lesions), within host growth (lesion size), the sporulation capacity (number of spores produced by lesion). Our results show the existence of GxG interactions on all measured traits and fungal fitness. We also observed that the varieties Ariete and CO39 have different resistance mechanisms; Ariete is good at controlling the success of infection of the parasite but is not able to control its growth when inside the leaf, while CO39 show the opposite pattern. We also found that Maratelli's resistance has been eroded. Finally, correlation analyses demonstrated that not all traits are positively correlated. In the meantime, we are searching for the genetic basis of the traits measured above. This is part of the Gandalf project. We performed a cross between two strains with contrasted trait values and obtained 158 progenies. The parents and progenies were inoculated on three rice varieties and the number of lesions, lesion size, and the number of spores per lesion were measured. The genome of all these strains is being sequenced to produce Single Nucleotide Polymorphism genotyping. A genetic map will be constructed and phenotypic data will be used to map QTLs for the three traits on the three varieties. Progresses on this work will be presented.